

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:11:15 ; Search time 42 Seconds  
(without alignments)  
166.285 Million cell updates/sec

Title: US09497591-1-LEDITED

Perfect score: 200

Sequence: 1 ANSFLXLRHSLRXRCIXX.....XXAKXIFVDVDTLAFWSKH 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*

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23: /SIDSI/gcgdata/geneeq/geneeqp-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneeq/geneeqp-emb1/AA2003.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	182	91.0	419	22	AAE08627 Human protein C de
2	182	91.0	419	22	AAE08628 Human protein C de
3	182	91.0	419	22	AAE08629 Human protein C de
4	182	91.0	419	22	AAE08627 Human protein C de
5	182	91.0	419	22	AAE08627 Human protein C de
6	176	88.0	44	20	AAE08627 Modified GLA domai
7	174	87.0	44	20	AAE08627 Modified GLA domai
8	174	87.0	44	20	AAE08627 Modified GLA domai
9	174	87.0	419	22	AAE08630 Human protein C de

10	174	87.0	419	22	AAE08627 Human protein C de
11	174	87.0	419	22	AAE08627 Human protein C de
12	170	85.0	45	23	ABB79950 Human protein C mu
13	168	84.0	44	20	AAE08627 Modified GLA domai
14	168	84.0	44	20	AAE08627 Modified GLA domai
15	168	84.0	44	20	AAE08627 Human protein C GL
16	168	84.0	44	20	AAE08627 Modified GLA domai
17	168	84.0	44	22	AAE08627 Human protein C ga
18	168	84.0	45	19	AAE08627 Partial human prot
19	168	84.0	45	23	ABB79947 Human protein C GL
20	168	84.0	415	21	AAE08627 Truncated human pr
21	168	84.0	419	14	AAE08627 Protein C (PC). H
22	168	84.0	419	19	AAE08627 Primary structure
23	168	84.0	419	22	AAE08625 Human mature wild
24	168	84.0	419	22	AAE08627 Wild-type human pr
25	168	84.0	419	22	AAE08627 Human protein C de
26	168	84.0	419	22	AAE08627 Human protein C de
27	168	84.0	419	22	AAE08627 Human protein C de
28	168	84.0	419	22	AAE08627 Human protein C de
29	168	84.0	419	23	AAU99002 Human protein C zy
30	168	84.0	419	23	AAU99003 Human protein C zy
31	168	84.0	419	23	AAU99004 Human protein C zy
32	168	84.0	419	23	AAU99005 Human protein C zy
33	168	84.0	419	23	AAU99006 Human protein C zy
34	168	84.0	419	23	AAU99007 Human protein C zy
35	168	84.0	419	23	AAU99008 Human protein C zy
36	168	84.0	419	23	AAU99009 Human protein C zy
37	168	84.0	419	23	AAU99010 Human protein C zy
38	168	84.0	419	23	AAU99011 Human protein C zy
39	168	84.0	419	23	AAU99012 Human protein C zy
40	168	84.0	419	23	AAU99013 Human protein C zy
41	168	84.0	419	23	AAU99014 Human protein C zy
42	168	84.0	419	23	AAU99015 Human protein C zy
43	168	84.0	419	23	AAU99016 Human protein C zy
44	168	84.0	419	23	AAU99017 Human protein C zy
45	168	84.0	419	23	AAU99018 Human protein C zy

#### ALIGNMENTS

RESULT 1  
AAE08627  
ID AAE08627 standard; Protein; 419 AA.

XX AC AAE08627;

XX DT 01-NOV-2001 (first entry)

XX DE Human protein C derivative #1.

XX DE Human; protein C derivative; anticoagulation activity; thrombosis;  
XX DE serpin inactivation; acute coronary syndrome; myocardial infarction;  
XX DE KW vascular occlusive disorder; hypercoagulable state; angina; sepsis;  
XX DE KW disseminated intravascular coagulation; DIC; burn; transplantation;  
XX DE KW sickle cell disease; viral haemorrhagic fever; protein C deficiency;  
XX DE KW haemolytic uremic syndrome; acute arterial thrombotic occlusion;  
XX DE KW thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.

XX OS Homo sapiens.

XX PN WO200159084-A1.

XX PD 16-AUG-2001.

XX PF 02-FEB-2001; 2001WO-US01221.

XX PR 11-FEB-2000; 2000US-0181948.

XX PR 14-MAR-2000; 2000US-0189199.

XX PA (ELIL) LILLY & CO ELI.

XX PI Gerlitz BE, Grinnell BW, Jones BE;



XX PA (BLIL ) LILLY & CO ELI.

XX PI Gerlitz BE, Grinnell BW, Jones BE;

XX XX WPI; 2001-514662/56.

DR N-PSDB; AAD15227.

XX XX Protein C derivative for treating acute coronary syndromes, vascular

PT occlusive disorders, thrombotic disorders and sepsis, comprises

PT substitutions at specified amino acid positions -

XX PS Claim 5; Page 48-49; 59pp; English.

XX XX The invention relates to human protein C derivatives and nucleic acid

CC molecules encoding such derivatives. These derivatives have increased

CC anticoagulation activity, resistance to serpin inactivation and

CC increased sensitivity to thrombin activation compared to wild type

CC protein C, and retains the biological activity of the wild type human

CC protein C. Protein C derivatives are useful in the manufacture of a

CC medicament for the treatment of acute coronary syndromes e.g. myocardial

CC infarction and unstable angina; and disease states predisposing to

CC thrombosis; vascular occlusive disorders and hypercoagulable states e.g.

CC disseminated intravascular coagulation (DIC), burns, transplantations,

CC thalassaemia, sickle cell disease, viral haemorrhagic fever and

CC haemolytic uremic syndrome; sepsis in combination with bacterial

CC permeability increasing protein; thrombotic disorders in combination

CC with an anti-platelet agent; protein C deficiency; acute arterial

CC thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral

CC or peripheral arteries or in vascular grafts in combination with a

CC thrombolytic agent. Nucleic acid molecules of the invention are useful

CC for treating humans with genetically predisposed prothrombotic disorders

CC by gene therapy. The present sequence is human protein C derivative.

XX SQ Sequence 419 AA;

Query Match 91.0%; Score 182; DB 22; Length 419;

Best Local Similarity 79.5%; Pred. No. 1e-21;

Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSXRCIXXICDPXAKXIFEDVDDTLAFWSKH 44

DB 1 ANSFLXLRHGSLEREICIEICDPFEAKEIFEDVDDTLAFWSKH 44

RESULT 4

AAB82675

ID AAB82675 standard; Protein; 419 AA.

XX AC AAB82675;

XX DT 15-OCT-2001 (first entry)

XX DE Human protein C derivative (S1LG/Q32E/N33D/L194S).

XX KW Protein C; human; coronary syndrome; thrombosis; angina;

XX KW myocardial infarction; vascular occlusive disorder;

XX KW hypercoagulation; sepsis; protein C deficiency; occlusion;

XX KW thromboembolism; stenosis; antibacterial; immunosuppressive;

XX KW thrombolytic; cardiac; antianginal; anticoagulant; therapy;

XX KW mutant; mutein.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 11

FT FT /note= "Ser in wild-type protein"

FT FT Misc-difference 32

FT FT /note= "Gln in wild-type protein"

FT FT Misc-difference 33

FT FT /note= "Asn in wild-type protein"

FT FT Misc-difference 194

FT FT /note= "Leu in wild-type protein"

FT FT 1..45

FT FT /note= "Gla domain"

FT FT Disulfide-bond 50..69

FT FT Disulfide-bond 59..64

FT FT Disulfide-bond 80..89

FT FT Disulfide-bond 98..109

FT FT Disulfide-bond 120..133

FT FT Disulfide-bond 141..277

FT FT Disulfide-bond 196..212

FT FT Disulfide-bond 331..345

FT FT Disulfide-bond 356..384

FT FT Cleavage-site 156..157

FT FT /note= "cleavage makes a 2-chain inactive

FT FT precursor (155-amino acid light chain

FT FT attached via a disulfide bond to a

FT FT 262-amino acid heavy chain)"

FT FT Modified-site 6

FT FT /note= "gamma-carboxylated"

FT FT Modified-site 7

FT FT /note= "gamma-carboxylated"

FT FT Modified-site 14

FT FT /note= "gamma-carboxylated"

FT FT Modified-site 16

FT FT /note= "gamma-carboxylated"

FT FT Modified-site 19

FT FT /note= "gamma-carboxylated"

FT FT Modified-site 20

FT FT /note= "gamma-carboxylated"

FT FT Modified-site 25

FT FT /note= "gamma-carboxylated"

FT FT Modified-site 26

FT FT /note= "gamma-carboxylated"

FT FT Peptide 158..169

FT FT /note= "activation peptide; removal activates the

FT FT 2-chain zymogen"

FT FT Cleavage-site 169..170

FT FT /note= "thrombin cleavage site"

FT FT Modified-site 29

FT FT /note= "N-glycosylated"

FT FT Modified-site 248

FT FT /note= "N-glycosylated"

FT FT Modified-site 313

FT FT /note= "N-glycosylated"

FT FT Modified-site 329

FT FT /note= "N-glycosylated"

XX XX WO200157193-A2.

XX XX 09-AUG-2001.

XX PD 19-JAN-2001; 2001WO-US00020.

XX PF 02-FEB-2000; 2000US-0179801.

XX PR 14-MAR-2000; 2000US-0189197.

XX XX (BLIL ) LILLY & CO ELI.

XX XX Gerlitz BE, Jones BE;

XX XX WPI; 2001-496919/54.

XX XX N-PSDB; AAB26363.

XX XX Novel human protein C derivative for treating, e.g., myocardial

XX XX infarction, unstable angina, sepsis, thrombotic disorders, acute

XX XX arterial thrombotic occlusion, and thromboembolism -

XX XX Claim 3; Page 52-53; 63pp; English.

XX XX The present sequence is that of a claimed human protein C

XX XX derivative in which Ser at amino acid position 11 of the mature

XX XX wild-type protein C sequence (see AAB82673) is substituted with

XX XX Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, and

CC Leu at position 194 with Ser. The protein is an example of protein  
 CC C derivatives of the invention that have at least 2 amino acid  
 CC substitutions, but which have increased anticoagulant activity and  
 CC resistance to inactivation by serpins compared with the wild-type  
 CC protein, while retaining the biological activity of the wild-type  
 CC protein. A method of producing the derivatives using recombinant  
 CC DNA methods is claimed. The protein C derivatives are useful for  
 CC treating coronary syndromes and disease states predisposing to  
 CC thrombosis (e.g. myocardial infarction and unstable angina),  
 CC vascular occlusive disorders and hypercoagulable states, sepsis (in  
 CC combination with bactericidal permeability increasing protein or  
 CC with tissue factor pathway inhibitor), thrombotic disorders (in  
 CC combination with an anti-platelet agent or by local delivery through  
 CC an intracoronary catheter), protein C deficiency, acute arterial  
 CC thrombotic occlusion, thromboembolism, or stenosis in coronary,  
 CC cerebral or peripheral arteries or in vascular grafts. Human  
 CC patients with genetically predisposed prothrombotic disorders may  
 CC be treated by gene therapy (all claimed).  
 XX  
 SQ Sequence 419 AA;

Query Match 91.0%; Score 182; DB 22; Length 419;  
 Best Local Similarity 79.5%; Pred. No. 1e-21;  
 Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSXKXCIXXICDPXKXKXIFEDVDVDTLAFWSKH 44  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1 ANSFLSELRHGSXKXERCEIEICDPFEAKXIFEDVDVDTLAFWSKH 44

RESULT 5  
 AAB82676  
 ID AAB82676 standard; Protein; 419 AA.

AC AAB82676;

XX 15-OCT-2001 (first entry)

XX Human protein C derivative (S11G/Q32E/N33D/L194S/T254S).

XX Protein C; human; coronary syndrome; thrombosis; angina;  
 KW myocardial infarction; vascular occlusive disorder;  
 KW hypercoagulation; sepsis; protein C deficiency; occlusion;  
 KW thromboembolism; stenosis; antibacterial; immunosuppressive;  
 KW thrombolytic; cardiant; antianginal; anticoagulant; therapy;  
 KW mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 11 /note= "Ser in wild-type protein"

FT Misc-difference 32 /note= "Gln in wild-type protein"

FT Misc-difference 33 /note= "Asn in wild-type protein"

FT Misc-difference 194 /note= "Leu in wild-type protein"

FT Misc-difference 254 /note= "Thr in wild-type protein"

FT Domain 1..45 /note= "Gla domain"

FT Disulfide-bond 50..69

FT Disulfide-bond 59..64

FT Disulfide-bond 80..89

FT Disulfide-bond 98..109

FT Disulfide-bond 120..133

FT Disulfide-bond 141..277

FT Disulfide-bond 196..212

FT Disulfide-bond 331..345

FT Disulfide-bond 356..384

FT Cleavage-site 156..157

/note= "cleavage makes a 2-chain inactive  
 precursor (155-amino acid light chain  
 attached via a disulfide bond to a  
 262-amino acid heavy chain)"

6 /note= "gamma-carboxylated"

7 /note= "gamma-carboxylated"

14 /note= "gamma-carboxylated"

16 /note= "gamma-carboxylated"

19 /note= "gamma-carboxylated"

20 /note= "gamma-carboxylated"

25 /note= "gamma-carboxylated"

26 /note= "gamma-carboxylated"

158..169 /note= "gamma-carboxylated"

/note= "activation peptide; removal activates the  
 2-chain zymogen"

169..170 /note= "thrombin cleavage site"

29 /note= "N-glycosylated"

248 /note= "N-glycosylated"

313 /note= "N-glycosylated"

329 /note= "N-glycosylated"

/note= "N-glycosylated"

WO200157193-A2.

09-AUG-2001.

19-JAN-2001; 2001WO-US00020.

02-FEB-2000; 2000US-0179801.

14-MAR-2000; 2000US-0189197.

(ELIL ) LILLY & CO ELI.

Gerlitz BE, Jones BE;

WPI; 2001-496919/54.

N-PSDB; AAH26364.

Novel human protein C derivative for treating, e.g., myocardial  
 infarction, unstable angina, sepsis, thrombotic disorders, acute  
 arterial thrombotic occlusion, and thromboembolism -

Claim 4; Page 53-54; 63pp; English.

The present sequence is that of a claimed human protein C derivative  
 in which Ser at position 11 of the mature wild-type protein C  
 sequence (see AAB82673) is substituted with Gly, Gln at position 32  
 with Glu, Asn at position 33 with Asp, Leu at position 194 with Ser,  
 and Thr at position 254 with Ser. It is an example of protein C  
 derivatives of the invention that have at least 2 amino acid  
 substitutions, but which have increased anticoagulant activity and  
 resistance to inactivation by serpins compared with the wild-type  
 protein, while retaining the biological activity of the wild-type  
 protein. A method of producing the derivatives using recombinant  
 DNA methods is claimed. The protein C derivatives are useful for  
 treating coronary syndromes and disease states predisposing to  
 thrombosis (e.g. myocardial infarction and unstable angina),  
 vascular occlusive disorders and hypercoagulable states, sepsis (in  
 combination with bactericidal permeability increasing protein or  
 with tissue factor pathway inhibitor), thrombotic disorders (in  
 combination with an anti-platelet agent or by local delivery through



```
XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
KW therapy.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 1..44
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
XX
XX WO9920767-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Nelsestuen GL;
XX
XX WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
XX
XX Claim 9; Page 82; 86pp; English.
XX
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
XX _Sequence 44 AA;
XX
XX Query Match 87.0%; Score 174; DB 20; Length 44;
XX Best Local Similarity 97.7%; Pred. No. 1.9e-21;
XX Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 ANSFLXLLRHGSLRXRCIXXICDPXXAKXIFEDVDDTLAFWSKH 44
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 1 ANSFLXLLRHGSLRXRCIXXICDPXXAKXIFEDVDDTLAFWSKH 44
XX
XX RESULT 9
XX AAE08630
XX ID AAE08630 standard; Protein; 419 AA.
XX
XX AC AAE08630;
XX
XX 01-NOV-2001 (first entry)
XX
XX Human protein C derivative #4.
XX
XX Human; protein C derivative; anticoagulation activity; thrombosis;
KW serpin inactivation; acute coronary syndrome; myocardial infarction;
KW vascular occlusive disorder; hypercoagulable state; angina; sepsis;
KW disseminated intravascular coagulation; DIC; burn; transplantation;
KW sickle cell disease; viral haemorrhagic fever; protein C deficiency;
KW haemolytic uremic syndrome; acute arterial thrombotic occlusion;
KW thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
XX
XX Homo sapiens.
OS
XX
XX WO200159084-A1.
XX
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PD 16-AUG-2001.
XX
XX 02-FEB-2001; 2001WO-US01221.
XX
XX 11-FEB-2000; 2000US-0181948.
PR 14-MAR-2000; 2000US-0189199.
XX
XX (ELIL ) LILLY & CO ELI.
XX
XX Gerlitz BE, Grinnell BW, Jones BE;
PI WPI; 2001-514662/56.
XX DR N-PSDB; AAD15228.
XX
XX Protein C derivative for treating acute coronary syndromes, vascular
PT occlusive disorders, thrombotic disorders and sepsis, comprises
PT substitutions at specified amino acid positions -
XX
XX Claim 6; Page 50-51; 59pp; English.
XX
XX The invention relates to human protein C derivatives and nucleic acid
CC molecules encoding such derivatives. These derivatives have increased
CC anticoagulation activity, resistance to serpin inactivation and
CC increased sensitivity to thrombin activation compared to wild type
CC protein C, and retains the biological activity of the wild type human
CC protein C. Protein C derivatives are useful in the manufacture of a
CC medicament for the treatment of acute coronary syndromes e.g. myocardial
CC infarction and unstable angina, and disease states predisposing to
CC thrombosis; vascular occlusive disorders and hypercoagulable states e.g.
CC disseminated intravascular coagulation (DIC), burns, transplantations,
CC thalassaemia, sickle cell disease, viral haemorrhagic fever and
CC permeability increasing protein; thrombotic disorders in combination
CC with an anti-platelet agent; protein C deficiency; acute arterial
CC thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral
CC or peripheral arteries or in vascular grafts in combination with a
CC thrombolytic agent. Nucleic acid molecules of the invention are useful
CC for treating humans with genetically predisposed prothrombotic disorders
CC by gene therapy. The present sequence is human protein C derivative.
XX
XX _Sequence 419 AA;
XX
XX Query Match 87.0%; Score 174; DB 22; Length 419;
XX Best Local Similarity 77.3%; Pred. No. 2.2e-20;
XX Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
XX
XX QY 1 ANSFLXLLRHGSLRXRCIXXICDPXXAKXIFEDVDDTLAFWSKH 44
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 1 ANSFLXLLRHGSLRXRCIXXICDPXXAKXIFEDVDDTLAFWSKH 44
XX
XX RESULT 10
XX AAB82677
XX ID AAB82677 standard; Protein; 419 AA.
XX
XX AC AAB82677;
XX
XX 15-OCT-2001 (first entry)
XX
XX Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S).
XX
XX Protein C; human; coronary syndrome; thrombosis; angina;
KW myocardial infarction; vascular occlusive disorder;
KW hypercoagulation; sepsis; protein C deficiency; occlusion;
KW thromboembolism; stenosis; antibacterial; immunosuppressive;
KW thrombolytic; cardiatic; antianginal; anticoagulant; therapy;
KW mutant; mutein.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 10
FT
```

FT Misc-difference 11 /note= "His in wild-type protein"  
 FT Misc-difference 32 /note= "Ser in wild-type protein"  
 FT Misc-difference 33 /note= "Gln in wild-type protein"  
 FT Misc-difference 194 /note= "Asn in wild-type protein"  
 FT Domain 1..45 /note= "Leu in wild-type protein"  
 FT Disulfide-bond 50..69 /note= "Gla domain"  
 FT Disulfide-bond 59..64  
 FT Disulfide-bond 80..89  
 FT Disulfide-bond 98..109  
 FT Disulfide-bond 120..133  
 FT Disulfide-bond 141..277  
 FT Disulfide-bond 196..212  
 FT Disulfide-bond 331..345  
 FT Disulfide-bond 356..384  
 FT Cleavage-site 156..157  
 FT /note= "Cleavage makes a 2-chain inactive precursor (155-amino acid light chain attached via a disulfide bond to a 262-amino acid heavy chain)"  
 FT Modified-site 6 /note= "gamma-carboxylated"  
 FT Modified-site 7 /note= "gamma-carboxylated"  
 FT Modified-site 14 /note= "gamma-carboxylated"  
 FT Modified-site 16 /note= "gamma-carboxylated"  
 FT Modified-site 19 /note= "gamma-carboxylated"  
 FT Modified-site 20 /note= "gamma-carboxylated"  
 FT Modified-site 25 /note= "gamma-carboxylated"  
 FT Modified-site 26 /note= "gamma-carboxylated"  
 FT Peptide 158..169 /note= "gamma-carboxylated"  
 FT /note= "activation peptide; removal activates the 2-chain zymogen"  
 FT Cleavage-site 169..170 /note= "thrombin cleavage site"  
 FT Modified-site 29 /note= "N-glycosylated"  
 FT Modified-site 248 /note= "N-glycosylated"  
 FT Modified-site 313 /note= "N-glycosylated"  
 FT Modified-site 329 /note= "N-glycosylated"  
 FT WO200157193-A2.  
 PN  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 19-JAN-2001; 2001WO-US00020.  
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 PR 02-FEB-2000; 2000US-0179801.  
 PR 14-MAR-2000; 2000US-0189197.  
 XX  
 PA (ELIL ) LILLY & CO ELI.  
 XX  
 PI Gerlitz BE, Jones BE;  
 XX  
 DR WPI: 2001-496919/54.  
 DR N-PSDB; AAH26365.  
 XX  
 PT Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute

PT arterial thrombotic occlusion, and thromboembolism -  
 XX  
 PS Claim 5; Page 54-55; 63pp; English.  
 CC  
 CC The present sequence is that of a claimed human protein C derivative in which His at position 10 of the mature wild-type protein C sequence (see AAB82673) is substituted with Gln, Ser at position 11 with Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, CC and Leu at position 194 with Ser. It is an example of protein C CC derivatives of the invention that have at least 2 amino acid CC substitutions, but which have increased anticoagulant activity and CC resistance to inactivation by serpins compared with the wild-type CC protein, while retaining the biological activity of the wild-type CC protein. A method of producing the derivatives using recombinant CC DNA methods is claimed. The protein C derivatives are useful for CC treating coronary syndromes and disease states predisposing to CC thrombosis (e.g. myocardial infarction and unstable angina), CC vascular occlusive disorders and hypercoagulable states, sepsis (in CC combination with bactericidal permeability increasing protein or CC with tissue factor pathway inhibitor), thrombotic disorders (in CC combination with an anti-platelet agent or by local delivery through CC an intracoronary catheter), protein C deficiency, acute arterial CC thrombotic occlusion, thromboembolism, or stenosis in coronary, CC cerebral or peripheral arteries or in vascular grafts. Human CC patients with genetically predisposed prothrombotic disorders may CC be treated by gene therapy (all claimed).  
 XX  
 SQ Sequence 419 AA;  
 Query Match 87.0%; Score 174; DB 22; Length 419;  
 Best Local Similarity 77.3%; Pred. No. 2.2e-20;  
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 ANSFLXLLRHGSLXRCIXXICDFXAXXIFEDVDDTLAFWSKH 44  
 DB 1 ANSFLLELRQGSLEECIEICDFEAKEIFEDVDDTLAFWSKH 44  
 RESULT 11  
 AAB82678  
 ID AAB82678 standard; Protein; 419 AA.  
 XX  
 AC AAB82678;  
 XX  
 DT 15-OCT-2001 (first entry)  
 XX  
 DE Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S/T254S).  
 KW Protein C; human; coronary syndrome; thrombosis; angina;  
 KW myocardial infarction; vascular occlusive disorder;  
 KW hypercoagulation; sepsis; protein C deficiency; occlusion;  
 KW thromboembolism; stenosis; antibacterial; immunosuppressive;  
 KW thrombolytic; cardiant; antianginal; anticoagulant; therapy;  
 KW mutant; mutein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 10 /note= "His in wild-type protein"  
 FT Misc-difference 11 /note= "Ser in wild-type protein"  
 FT Misc-difference 32 /note= "Gln in wild-type protein"  
 FT Misc-difference 33 /note= "Asn in wild-type protein"  
 FT Misc-difference 194 /note= "Leu in wild-type protein"  
 FT Misc-difference 254 /note= "Thr in wild-type protein"  
 FT Domain 1..45 /note= "Gla domain"  
 FT







Query Match 84.0%; Score 168; DB 20; Length 44;  
Best Local Similarity 95.5%; Pred. No. 1.9e-20;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRCIXXICDPXXAKXIFEDVDDTLAFWSKH 44  
|||||  
DB 1 ANSFLXXLRHGSIXRCIXXICDPXXAKXIFEDVDDTLAFWSKH 44  
|||||

## RESULT 15

AAV18303  
ID AAY18303 standard; peptide; 44 AA.

XX AAY18303;

DT 17-AUG-1999 (first entry)

XX Human protein C GLA domain.

XX GLA domain; vitamin K-dependent protein; clotting disorder;  
KW therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1..44  
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic  
FT acid"

XX W09920767-A1.

XX 29-APR-1999.

XX 20-OCT-1998; 98WO-US22152.

XX 23-OCT-1997; 97US-0955636.

XX (MINU ) UNIV MINNESOTA.

XX Nelsestuen GL;

XX WPI; 1999-288309/24.

XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
PT acid domain, useful for treating clotting disorders

XX Disclosure; Page 14; 86pp; English.

XX This sequence is the protein C GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the  
CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.

XX Sequence 44 AA;

Query Match 84.0%; Score 168; DB 20; Length 44;  
Best Local Similarity 93.2%; Pred. No. 1.9e-20;  
Matches 41; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRCIXXICDPXXAKXIFEDVDDTLAFWSKH 44  
|||||  
DB 1 ANSFLXXLRHGSIXRCIXXICDPXXAKXIFQNVDDTLAFWSKH 44  
|||||

Search completed: December 30, 2003, 09:18:18  
Job time : 43 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:16:41 ; Search time 21 Seconds  
(without alignments)  
201.496 Million cell updates/sec

Title: US09497591-LEDITED  
Perfect score: 200  
Sequence: 1 ANSFLXLRHGLXRCIXX.....XXAKXIFdVDTLAFWSKH 44  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	168	84.0	461	1 KXHU	protein C (activat
2	139	69.5	461	1 JX0210	protein C (activat
3	138	69.0	461	1 S18994	protein C (activat
4	121	60.5	456	1 KXBO	coagulation factor
5	113	56.5	482	1 EXRT	coagulation factor
6	109	54.5	492	1 EXBO	coagulation factor
7	108	54.0	488	1 EXHU	coagulation factor
8	100	50.0	443	2 I4932	coagulation factor
9	98	49.0	466	1 KFH07	coagulation factor
10	84.5	42.2	617	2 S10511	thrombin (EC 3.4.2
11	84.5	42.2	618	2 K35827	thrombin (EC 3.4.2
12	84	42.0	407	1 KFB07	coagulation factor
13	82	41.0	622	1 TBHU	coagulation factor
14	81	40.5	475	1 EXCH	coagulation factor
15	80	40.0	642	2 S53434	plasma protein S p
16	80	40.0	676	1 KXHUS	plasma protein S p
17	79	39.5	452	1 A30351	coagulation factor
18	79	39.5	459	2 JQ0419	coagulation factor
19	79	39.5	646	2 S38919	plasma protein S -
20	78	39.0	675	1 KXBOS	plasma protein S p
21	76	38.0	675	1 KXRTS	plasma protein S p
22	75	37.5	461	1 KFHU	coagulation factor
23	73	36.5	642	2 S53433	plasma protein S p
24	72	36.0	416	1 KFB0	coagulation factor
25	70	35.0	625	1 TBBO	thrombin (EC 3.4.2
26	69	34.5	675	1 KXMS	plasma protein S p
27	67.5	33.8	396	1 KXBOZ	plasma protein Z -
28	63.5	31.8	422	1 KXHUZ	plasma protein Z p
29	60	30.0	673	2 A48089	growth arrest-spec

ALIGNMENTS

RESULT 1

KXHU

protein C (activated) (EC 3.4.21.69) precursor - human  
N:Alternate names: autoprothrombin IIA; plasma protein C  
C:Species: Homo sapiens (man)  
C>Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text\_change 16-Jul-1999  
C:Accession: A22331; A25426; A21781; A23789; A00927  
R:Poster, D.C.; Yoshitake, S.; Davie, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985  
A:Title: The nucleotide sequence of the gene for human protein C.  
A:Reference number: A22331; MUID:85270390; PMID:2991887  
A:Accession: A22331  
A:Molecule type: DNA  
A:Residues: 1-461 <POS1>  
A:Cross-references: GB:M1128; NID:g190333; PIDN:AAA60166.1; PID:g190334  
R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.  
Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986  
A:Title: Evolution and organization of the human protein C gene.  
A:Reference number: A25426; MUID:86120978; PMID:3511471  
A:Accession: A25426  
A:Molecule type: DNA  
A:Residues: 1-445, 'L', 446-461 <PLU>  
A:Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332  
R:Poster, D.; Davie, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984  
A:Title: Characterization of a cDNA coding for human protein C.  
A:Reference number: A21781; MUID:84272714; PMID:6589623  
A:Accession: A21781  
A:Molecule type: mRNA  
A:Residues: 'O', 107-461 <POS2>  
A:Cross-references: GB:X02059; NID:g190322; PIDN:AAA60164.1; PID:g190323  
R:Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.  
Nucleic Acids Res. 13, 5233-5247, 1985  
A:Title: The structure and evolution of a 461 amino acid human protein C precursor and it  
A:Reference number: A23789; MUID:85269639; PMID:2991859  
A:Accession: A23789  
A:Molecule type: mRNA  
A:Residues: 1-461 <BEC>  
A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120  
R:Miletich, J.P.; Broze Jr., G.J.  
J. Biol. Chem. 265, 11397-11404, 1990  
A:Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation me  
A:Reference number: A44605; MUID:90293094; PMID:1694179  
A:Contents: annotation; carbohydrate binding sites; activation peptide  
A:Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not  
R:Harris, R.J.; Ling, V.T.; Spellman, M.W.  
J. Biol. Chem. 267, 5102-5107, 1992  
A:Title: O-linked fucose is present in the first epidermal growth factor domain of factor  
A:Reference number: A44606; MUID:92184750; PMID:1544894  
A:Contents: annotation; beta-hydroxyaspartic acid  
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in  
ivation of factor Va is strongly enhanced by complexing with protein S. Protein C also f

growth potentiati  
growth arrest-spec  
probable MAP kinase  
probable MAP kinase  
probable MAP kinase  
probable MAP kinase  
hypothetical prote  
hypothetical prote  
alcohol dehydrogen  
primosomal replica  
protein-tyrosine k  
hypothetical prote  
hypothetical prote  
ammonium transport  
VSG expression sit  
protein-tyrosine k  
tyrosine kinase re



J. Biol. Chem. 257, 12170-12179, 1982  
A;Title: Amino acid sequence of the light chain of bovine protein C.  
A;Reference number: A18385; MUID:83007325; PMID:6896876  
A;Accession: A18385  
A;Molecule type: protein  
A;Residues: 40-194 <PER>  
A;Note: 82-Lys was also found  
R;Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.  
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983  
A;Title: Beta-Hydroxyaspartic acid in vitamin K-dependent protein C.  
A;Reference number: A19316; MUID:83189769; PMID:6572939  
A;Contents: annotation; revision to residue 110  
R;Stenflo, J.; Fernlund, P.  
J. Biol. Chem. 257, 12180-12190, 1982  
A;Title: Amino acid sequence of the heavy chain of bovine protein C.  
A;Reference number: A18386; MUID:83007326; PMID:6896877  
A;Accession: A18386  
A;Molecule type: protein  
A;Residues: 197-454, 'PV' <STE>  
R;Esmon, N.L.; DeBault, L.E.; Esmon, C.T.  
J. Biol. Chem. 258, 5548-5553, 1983  
A;Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless protein C.  
A;Reference number: A37541; MUID:83213513; PMID:6304092  
A;Contents: annotation; activation; calcium binding  
R;Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.  
J. Biol. Chem. 258, 5554-5560, 1983  
A;Title: Structural changes required for activation of protein C are induced by Ca2+ binding.  
A;Reference number: A37542; MUID:83213514; PMID:6406503  
A;Contents: annotation; activation; calcium binding  
C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that releases active protein C.  
C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is cleaved by a trypsin-like protease to form the active protein C.  
C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with the aid of the thrombin-thrombomodulin complex.  
C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin K-dependent modification of the glutamic acid residues.  
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C;Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding  
F;1-29/Domain: signal sequence (fragment) #status predicted <SIG>  
F;24-83/Domain: Gla domain homology <GLA>  
F;30-38/Domain: propeptide #status predicted <PRO>  
F;40-194/Product: protein C light chain #status experimental <LCH>  
F;98-128/Domain: EGF homology <EG1>  
F;137-172/Domain: EGF homology <EG2>  
F;197-456/Product: protein C heavy chain #status experimental <HCH>  
F;211-440/Domain: trypsin homology <TRY>  
F;45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted  
F;110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F;119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #status predicted  
F;136,289,350/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;252,298,397/Active site: His, Asp, Ser #status predicted  
F;366/Binding site: carboxylate (Asn) (covalent) #status predicted  
Query Match 60.5%; Score 121; DB 1; Length 456;  
Best Local Similarity 50.0%; Pred. No. 1.6e-11;  
Matches 21; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 ANSFLXLRGSLRXRCIXXCDFXXAKXIFEDVDDTLAFWS 42  
Db 40 ANSFLRLPGNVERECSEVCEFEAREIFQNTEDTMAFWS 81  
RESULT 5  
EXRT  
coagulation factor Xa (EC 3.4.21.6) precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text\_change 08-Dec-2000  
A;Accession: S49075; JC4670; PS0190; I62745  
R;Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.  
Thromb. Res. 80, 63-73, 1995  
A;Title: Evidence for competition between vitamin K-dependent clotting factors for intracellular calcium.  
A;Reference number: A58498; MUID:96093366; PMID:8578539

A;Accession: S49075  
A;Molecule type: mRNA  
A;Residues: 1-482 <STAL>  
A;Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601  
A;Note: submitted to the EMBL Data Library, June 1994  
R;Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.  
Gene 169, 269-273, 1996  
A;Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.  
A;Reference number: JC4670; MUID:96194815; PMID:8647460  
A;Accession: JC4670  
A;Molecule type: mRNA  
A;Residues: 1-482 <STA2>  
A;Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601  
A;Experimental source: Cos-1 cell  
R;Enjiyoji, K.; Miyazaki, K.; Kato, H.  
J. Biochem. 109, 890-898, 1991  
A;Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plasma.  
A;Reference number: PS0190; MUID:92041742; PMID:1718949  
A;Accession: PS0191  
A;Molecule type: protein  
A;Residues: 41-58, 'X', 60-65 <ENJ1>  
A;Accession: PS0190  
A;Molecule type: protein  
A;Residues: 183-186, 'X', 188-207 <ENJ2>  
R;Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.  
Eur. J. Haematol. 52, 162-168, 1994  
A;Title: Analysis of the partial nucleotide sequences and deduced primary structures of the human factor Xa.  
A;Reference number: I46196; MUID:94222160; PMID:8168596  
A;Accession: I62745  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 295-383, 'G', 385-455 <MUR>  
A;Cross-references: GB:D21215; NID:G415309; PIDN:BAA04756.1; PID:G455396  
C;Function:  
A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor V.  
A;Pathway: blood coagulation  
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic acid  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-40/Domain: propeptide #status predicted <PRO>  
F;41-179/Product: coagulation factor X light chain #status predicted <LCH>  
F;90-121/Domain: EGF homology <EG1>  
F;129-164/Domain: EGF homology <EG2>  
F;183-482/Product: coagulation factor X heavy chain #status predicted <HCH>  
F;232-482/Product: activation peptide #status predicted <APT>  
F;232-460/Domain: trypsin homology <TRY>  
F;46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted  
F;57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-402,411-421/Disulfide bonds: #status predicted  
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F;187/Binding site: carboxylate (Asn) (covalent) #status experimental  
F;208/Binding site: carboxylate (Thr) (covalent) #status predicted  
F;218/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status predicted  
F;274,320,417/Active site: His, Asp, Ser #status predicted  
Query Match 56.5%; Score 113; DB 1; Length 482;  
Best Local Similarity 43.2%; Pred. No. 3.4e-10;  
Matches 19; Conservative 9; Mismatches 16; Indels 0; Gaps 0;  
Qy 1 ANSFLXLRGSLRXRCIXXCDFXXAKXIFEDVDDTLAFWSGH 44  
Db 41 ANSFPEIKKGNLRECEVEICSEFEAREVFEEDNEKTEFWNKY 84  
RESULT 6  
EXBO  
coagulation factor Xa (EC 3.4.21.6) precursor - bovine  
N;Alternate names: Stuart factor  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 24-Apr-1984 #sequence\_revision 17-Mar-1987 #text\_change 16-Jul-1999



F;103/Modified site: erythro-beta-hydroxypartac acid (Asp) #status experimental  
F;199,211/Binding site: carbohydtrate (Thr) (covalent) #status experimental  
F;221,231/Binding site: carbohydtrate (Asn) (covalent) #status experimental  
F;234-235/Cleavage site: Arg-ile (Coagulation factor IXa, Coagulation factor VIIa) #statu  
F;276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 54.0%; Score 108; DB 1; Length 488;  
Best Local Similarity 43.2%; Pred. No. 2.2e-09;  
Matches 19; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSILKRXICIXXICDFFXXAKXIFEDVDVDTTLAFWSKH 44  
||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
Db 41 ANSFLEMKKGHLRECMETCTSYEARVEVPDSDKTNEFWNKY 84  
||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 8  
I46932  
C;Species: Oryctolagus cuniculus - rabbit  
C;Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 12-Feb-1999  
C;Accession: I46932  
R;Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.  
Thromb. Res. 69, 231-238, 1993  
A;Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII  
A;Reference number: I46932; MUID:93190306; PMID:8383365  
A;Accession: I46932  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-443 <BRO>  
A;Cross-references: GB:S56300; NID:g266294; PID:g266295  
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
F;24-83/Domain: Gla domain homology <GLA>  
F;89-120/Domain: EGF homology <EGI>  
F;130-166/Domain: EGF homology <EG2>  
F;192-425/Domain: trypsin homology <TRY>

Query Match 50.0%; Score 100; DB 2; Length 443;  
Best Local Similarity 46.3%; Pred. No. 3.9e-08;  
Matches 19; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSILKRXICIXXICDFFXXAKXIFEDVDVDTTLAFW 41  
||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
Db 40 ANSFLEELPGSUERECKEELCSFEAREVFPQSTERTKQFW 80  
||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 9  
KFHU7  
Coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human  
C;Species: Homo sapiens (man)  
C;Date: 19-May-1989 #sequence\_revision 19-May-1994 #text\_change 08-Dec-2000  
C;Accession: A28322; A23819; K31186; B31186; S63524  
R;O'Hara, P. J.; Grant, F. J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murra  
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987  
A;Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depende  
A;Reference number: A28322; MUID:87260948; PMID:3037537  
A;Accession: A28322  
A;Molecule type: DNA  
A;Residues: 1-466 <OKHA>  
A;Cross-references: GB:J02933; NID:g180333; PIDN:AAA51983.1; PID:g180334  
R;Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C.  
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986  
A;Title: Characterization of a cDNA coding for human factor VII.  
A;Reference number: A23819; MUID:86205965; PMID:3486420  
A;Accession: A23819  
A;Molecule type: mRNA  
A;Residues: 1-466 <HAG>  
A;Cross-references: GB:M13232; NID:g182799; PIDN:AAA88040.1; PID:g182801  
R;Thim, L.; Bjorn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.F.  
Biochemistry 27, 7785-7793, 1988  
A;Title: Amino acid sequence and posttranslational modifications of human factor VII-a fr  
A;Reference number: A90539; MUID:89088153; PMID:3264725  
A;Accession: A31186  
A;Molecule type: protein











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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:11:16 ; Search time 12 Seconds  
(without alignments)  
172.431 Million cell updates/sec

Title: US09497591-LEDITED

Perfect score: 200

Sequence: 1 ANSFLXLRHGLRXRCIXX.....XXAKXIFedVDDTLAFWSKH 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	168	84.0	461	1 PRTC_HUMAN	P04070 homo sapien
2	139	69.5	461	1 PRTC_MOUSE	F33587 mus musculus
3	138	69.0	461	1 PRTC_RAT	F31394 rattus norv
4	137	68.5	458	1 PRTC_RABIT	Q28661 oryctolagus
5	122	61.0	459	1 PRTC_PIG	O9glp2 sus scrofa
6	121	60.5	456	1 PRTC_BOVIN	P00745 bos taurus
7	109	54.5	432	1 FA10_BOVIN	P00743 bos taurus
8	108	54.0	488	1 FA10_HUMAN	P00742 homo sapien
9	102	51.0	231	1 TMG3_HUMAN	O9bzd7 homo sapien
10	101	50.5	490	1 FA10_RABIT	O19045 oryctolagus
11	100	50.0	444	1 FA7_RABIT	P98139 oryctolagus
12	98	49.0	466	1 FA7_HUMAN	P08709 homo sapien
13	87	43.5	218	1 TMG1_HUMAN	O14668 homo sapien
14	84.5	42.2	617	1 THRB_RAT	P18292 rattus norv
15	84.5	42.2	618	1 THRB_MOUSE	P19221 mus musculus
16	84	42.0	226	1 TMG4_HUMAN	O9bzd6 homo sapien
17	84	42.0	407	1 FA7_BOVIN	P22457 bos taurus
18	82	41.0	622	1 THRE_HUMAN	P00734 homo sapien
19	81	40.5	376	1 FA10_TROCA	P81428 tropidechis
20	81	40.5	475	1 FA10_CHICK	P25155 gallus gall
21	80	40.0	649	1 PRTS_MACMU	Q28520 macaca mula
22	80	40.0	676	1 PRTS_HUMAN	P07225 homo sapien
23	79	39.5	446	1 FA7_MOUSE	P70375 mus musculus
24	79	39.5	452	1 FA9_CANFA	P19540 canis famil
25	79	39.5	459	1 FA9_MOUSE	P16294 mus musculus
26	79	39.5	646	1 PRTS_RABIT	P98118 oryctolagus
27	78	39.0	675	1 PRTS_BOVIN	P07224 bos taurus
28	76	38.0	675	1 PRTS_RAT	P53813 rattus norv
29	75	37.5	461	1 FA9_HUMAN	P00740 homo sapien
30	72	36.0	416	1 FA9_BOVIN	P00741 bos taurus
31	70	35.0	625	1 THRB_BOVIN	P00735 bos taurus
32	69	34.5	675	1 PRTS_MOUSE	Q08761 mus musculus
33	67.5	33.8	396	1 PRTC_BOVIN	P00744 bos taurus

RESULT 1  
PRTC\_HUMAN  
ID PRTC\_HUMAN STANDARD; PRT; 461 AA.  
AC P04070; Q15189; Q15190; Q16001;  
DT 01-NOV-1986 (Rel. 03, Created)  
DT 01-NOV-1986 (Rel. 03, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)  
DE (Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).  
GN PROC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85270390; PubMed=2991887;  
RA Foster D.C., Yoshitake S., Davie E.W.;  
RT "The nucleotide sequence of the gene for human protein C.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85269639; PubMed=2991859;  
RA Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree G.R., Long G.L.;  
RT "The structure and evolution of a 461 amino acid human protein C precursor and its messenger RNA, based upon the DNA sequence of cloned human liver cDNAs";  
RL Nucleic Acids Res. 13:5233-5247(1985).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86120978; PubMed=3511471;  
RA Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.;  
RT "Evolution and organization of the human protein C gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q., Nickerson D.A.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 106-461 FROM N.A.  
RX MEDLINE=84272714; PubMed=6589623;  
RA Foster D.C., Davie E.W.;  
RT "Characterization of a cDNA coding for human protein C";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).  
RN [6]  
RP CARBOHYDRATE-LINKAGE SITE ASN-371.  
RX MEDLINE=90293094; PubMed=1694179;  
RA Milewich J.P., Broze G.J. Jr.;  
RT "Beta protein C is not glycosylated at asparagine 329. The rate of translation may influence the frequency of usage at asparagine-X-cysteine sites.";  
RL J. Biol. Chem. 265:11397-11404(1990).  
RN [7]

#### ALIGNMENTS

34 64 32.0 202 1 TMG2\_HUMAN  
35 63.5 31.8 400 1 PRTC\_HUMAN  
36 51 25.5 501 1 MKC1\_CANAL  
37 49.5 24.8 941 1 VP11\_HUMAN  
38 49.5 24.8 941 1 VP11\_MOUSE  
39 49 24.5 558 1 ALKJ\_PSEOL  
40 49 24.5 730 1 PRIA\_HAEIN  
41 49 24.5 1363 1 VGR3\_MOUSE  
42 48 24.0 1235 1 CYA4\_TRYBB  
43 48 24.0 1298 1 VGR3\_HUMAN  
44 48 24.0 2812 1 ZAN\_HUMAN  
45 47 23.5 244 1 T2E5\_ECOLI

O14669 homo sapien  
P22891 homo sapien  
P43068 candida alb  
Q9h270 homo sapien  
Q9l866 mus musculus  
Q00593 pseudomonas  
P44647 haemophilus  
P35917 mus musculus  
Q26721 trypanosoma  
P35916 homo sapien  
Q9Y493 homo sapien  
P04390 escherichia

RP HYDROXYLATION.  
 RX MEDLINE=92184750; PubMed=1544894;  
 RA Harris R.J., Ling V.T., Spellman M.W.;  
 RT "O-linked fucose is present in the first epidermal growth factor  
 RT domain of factor XII but not protein C.";  
 RL J. Biol. Chem. 267:5102-5107(1992).  
 RN [8]  
 RP 3D-STRUCTURE MODELING OF 175-450.  
 RX MEDLINE=94272342; PubMed=8003977;  
 RA Fisher C.L., Greengard J.S., Griffin J.H.;  
 RT "Models of the serine protease domain of the human antithrombotic  
 RT plasma factor activated protein C and its zymogen.";  
 RL Protein Sci. 3:588-599(1994).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.  
 RX MEDLINE=97157472; PubMed=9003757;  
 RA Mather T., Oganessyan V., Hof P., Huber R., Foundling S., Esmen C.,  
 RA Bode W.;  
 RT "The 2.8 A crystal structure of Gla-domainless activated protein C.";  
 RL EMBO J. 15:6822-6831(1996).  
 RN [10]  
 RP REVIEW ON PROC VARIANTS.  
 RX MEDLINE=93190290; PubMed=8446940;  
 RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,  
 RA Sala N., Cooper D.N.;  
 RT "Protein C deficiency: a database of mutations. For the Protein C & S  
 RT Subcommittee of the Scientific and Standardization Committee of the  
 RT International Society on Thrombosis and Haemostasis.";  
 RL Thromb. Haemost. 69:77-84(1993).  
 RN [11]  
 RP VARIANT CYS-444.  
 RX MEDLINE=87204221; PubMed=2437584;  
 RA Romeo G., Hassan H.J., Staemfli S., Roncuzzi L., Cianetti L.,  
 RA Leonardi A., Vicence V., Mannucci P.M., Bertina R.M., Peschle C.,  
 RA Cortese R.;  
 RT "Hereditary thrombophilia: identification of nonsense and missense  
 RT mutations in the protein C gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).  
 RN [12]  
 RP VARIANT TRP-211 (LONDON-1).  
 RX MEDLINE=90098906; PubMed=2602169;  
 RA Grundy C.B., Chitollie A., Talbot S., Bevan D., Kakkar V.V.,  
 RA Cooper D.N.;  
 RT "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in  
 RT the protein C gene causing thrombosis.";  
 RL Nucleic Acids Res. 17:10513-10513(1989).  
 RN [13]  
 RP VARIANT CYS-272.  
 RX MEDLINE=91329836; PubMed=1868249;  
 RA Reitsma P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.;  
 RT "The spectrum of genetic defects in a panel of 40 Dutch families with  
 RT symptomatic protein C deficiency type I: heterogeneity and founder  
 RT effects.";  
 RL Blood 78:890-894(1991).  
 RN [14]  
 RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.  
 RX MEDLINE=92190481; PubMed=1347706;  
 RA Bovill E.G., Tomczak J.A., Grant B., Bhushan P., Pillemer E.,  
 RA Rainville I.R., Long G.L.;  
 RT "Protein C Vermont: symptomatic type II protein C deficiency  
 RT associated with two GLA domain mutations.";  
 RL Blood 79:1456-1465(1992).  
 RN [15]  
 RP VARIANT ASP-418 (HONG KONG-2).  
 RX MEDLINE=92305321; PubMed=1611081;  
 RA Sugahara Y., Miura O., Yuen P., Aoki N.;  
 RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C  
 RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and  
 RT a missense mutation.";  
 RL Blood 80:126-133(1992).  
 RN [16]  
 RP VARIANT LEU-289.  
 RX MEDLINE=92380660; PubMed=1511988;

RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;  
 RT "A novel homozygous missense mutation in the protein C (PROC) gene  
 RT causing recurrent venous thrombosis.";  
 RL Hum. Genet. 89:683-684(1992).  
 RN [17]  
 RP VARIANTS GLN-220 AND TRP-220.  
 RX MEDLINE=92380661; PubMed=1511989;  
 RA Grundy C.B., Schulman S., Tengborn L., Kakkar V.V., Cooper D.N.;  
 RT "Two different missense mutations at Arg 178 of the protein C (PROC)  
 RT gene causing recurrent venous thrombosis.";  
 RL Hum. Genet. 89:685-686(1992).  
 RN [18]  
 RP VARIANT GLN-220.  
 RX MEDLINE=93250852; PubMed=1301959;  
 RA Gandrille S., Vidaud M., Aïach M., Alhenc-Gelas M., Fischer A.M.,  
 RA Gouault-Heilman M., Toulon P., Fiesinger J.N., Goossens M.;  
 RT "Two novel mutations responsible for hereditary type I protein C  
 RT deficiency: characterization by denaturing gradient gel  
 RT electrophoresis.";  
 RL Hum. Mutat. 1:491-500(1992).  
 RN [19]  
 RP VARIANT SER-334.  
 RX MEDLINE=92276939; PubMed=1593215;  
 RA Yamamoto K., Matsushita T., Suglura I., Takamatsu J., Iwasaki E.,  
 RA Wada H., Deguchi K., Shirakawa S., Saito H.;  
 RT "Homozygous protein C deficiency: identification of a novel missense  
 RT mutation that causes impaired secretion of the mutant protein C.";  
 RL J. Lab. Clin. Med. 119:682-689(1992).  
 RN [20]  
 RP VARIANTS TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.  
 RX MEDLINE=93313192; PubMed=8324221;  
 RA Gandrille S., Alhenc-Gelas M., Gaussem P., Aillaud M.-F., Dupuy E.,  
 RA Juhan-Vague I., Aïach M.;  
 RT "Five novel mutations located in exons III and IX of the protein C  
 RT gene in patients presenting with defective protein C anticoagulant  
 RT activity.";  
 RL Blood 82:159-168(1993).  
 RN [21]  
 RP VARIANTS GLY-14; GLN-211; TYR-244; GLN-253; LEU-321; CYS-328; ILE-385;  
 RP THR-388 AND VAL-388.  
 RX MEDLINE=93271391; PubMed=8499565;  
 RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,  
 RA Bertina R.M.;  
 RT "Twelve novel and two recurrent mutations in 14 Austrian families  
 RT with hereditary protein C deficiency.";  
 RL Blood Coagul. Fibrinolysis 4:273-280(1993).  
 RN [22]  
 RP VARIANT TRP-57.  
 RX MEDLINE=93271396; PubMed=8499568;  
 RA Millar D.S., Grundy C.B., Bignell P., Moffat E.H., Martin R.,  
 RA Kakkar V.V., Cooper D.N.;  
 RT "A Gla domain mutation (Arg 15-->Trp) in the protein C (PROC) gene  
 RT causing type 2 protein C deficiency and recurrent venous  
 RT thrombosis.";  
 RL Blood Coagul. Fibrinolysis 4:345-347(1993).  
 RN [23]  
 RP VARIANTS ARG-145; LEU-210; TRP-211; THR-243; LEU-321; MET-340 AND  
 RP TYR-426.  
 RX MEDLINE=94122329; PubMed=8292730;  
 RA Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C.,  
 RA Koerber M.A., Coughlin J., Griffin J.H.;  
 RT "Genetic mutations in ten unrelated American patients with  
 RT symptomatic type I protein C deficiency.";  
 RL Blood Coagul. Fibrinolysis 4:791-796(1993).  
 RN [24]  
 RP VARIANT SER-423.  
 RX MEDLINE=94001606; PubMed=8398832;  
 RA Marchetti G., Patraccini P., Gemmati D., Castaman G., Rodeghiero F.,  
 RA Wacey A., Cooper D.N., Tuddenham E.G., Bernardi F.;  
 RT "Symptomatic type II protein C deficiency caused by a missense  
 RT mutation (Gly 381-->Ser) in the substrate-binding pocket.";  
 RL Br. J. Haematol. 84:285-289(1993).  
 RN [25]





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FT DISULFID 373 387 BY SIMILARITY.
FT DISULFID 398 426 BY SIMILARITY.
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 461 AA; 51912 MW; 8A4CF93664EDACD5 CRC64;

Query Match 69.0%; Score 138; DB 1; Length 461;
Best Local Similarity 59.1%; Pred. No. 8.7e-16;
Matches 26; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ANSLFLXLRGSLRXKICXIXICDPKXAKXIPEDVDDTLAFWSKH 44
Db 42 ANSLFEEVRAGSLRECMEBICDPFEAQEIFQNVEDTLAFWKY 85

RESULT 4
PRTC_RABIT STANDARD; PRT; 458 AA.
AC Q28661;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysis IIA) (Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment).
GN PROC.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Shen L., He X., Dahlback B.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIA.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; U49933; AAA2956.1; -
CC HSSP; P04070; 1PCU.
CC MEROPS; S01.218; -
CC InterPro; IPR000152; Asx_hydroxyl.
CC InterPro; IPR001314; Chymotrypsin.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_Like.
CC InterPro; IPR002383; GLA_Blood.

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DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; glr_1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT NON_TER 1 1
FT SIGNAL <1 27 BY SIMILARITY.
FT PROPEP 28 36 BY SIMILARITY.
FT CHAIN 37 458 VITAMIN K-DEPENDENT PROTEIN C.
FT CHAIN 37 192 PROTEIN C LIGHT CHAIN (BY SIMILARITY).
FT CHAIN 195 458 PROTEIN C HEAVY CHAIN (BY SIMILARITY).
FT PEPTIDE 195 209 ACTIVATION PEPTIDE (BY SIMILARITY).
FT SITE 209 210 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT DOMAIN 91 126 EGF-LIKE 1.
FT DOMAIN 130 170 EGF-LIKE 2.
FT DOMAIN 210 458 SERINE PROTEASE.
FT MOD_RES 42 42 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 43 43 (BY SIMILARITY).
FT MOD_RES 43 43 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 50 50 (BY SIMILARITY).
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FT MOD_RES 52 52 (BY SIMILARITY).
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FT MOD_RES 61 61 (BY SIMILARITY).
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FT MOD_RES 62 62 (BY SIMILARITY).
FT MOD_RES 62 62 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 65 65 (BY SIMILARITY).
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID
FT ACT_SITE 107 107 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 250 250 CHARGE RELAY SYSTEM.
FT ACT_SITE 296 296 CHARGE RELAY SYSTEM.
FT ACT_SITE 399 399 CHARGE RELAY SYSTEM.
FT DISULFID 53 58 BY SIMILARITY.
FT DISULFID 85 105 BY SIMILARITY.
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FT DISULFID 156 169 BY SIMILARITY.
FT DISULFID 177 316 INTERCHAIN (BY SIMILARITY).
FT DISULFID 235 251 BY SIMILARITY.
FT DISULFID 370 384 BY SIMILARITY.
FT DISULFID 395 423 BY SIMILARITY.
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 458 AA; 51087 MW; D75A5F90C8F29D7 CRC64;

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Query Match

68.5%; Score 137; DB 1; Length 458;



Best Local Similarity 59.1%; Pred. No. 1.3e-15;  
Matches 26; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 1 ANSLFLXLRGSLXRCIXICDFFXAKXIFEDVDDTLAFWSKH 44  
DB 37 ANSFLBELRPSLRECEVVECDLEAKEIFQSVDVDTLAFWKY 80

RESULT 5  
PRTC\_PIG STANDARD; PRT; 459 AA.

AC Q9GLP2;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)  
DE (Autoproteolysis IIA) (Anticoagulant protein C) (Blood coagulation factor XIV)  
GN PROC.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=21121490; PubMed=11229814;  
RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,  
RA Kim H.K.W.;  
RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional protein modeling of membrane binding sites and comparative anatomy of domains";  
RT Cell. Mol. Life Sci. 58:148-159(2001).  
CC -I- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.  
CC -I- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIa.  
CC -I- SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.  
CC -I- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
CC -I- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.  
CC -I- MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.  
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC -I- SIMILARITY: Contains 2 EGF-like domains.

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EMBL: AF191307; AAC28380.1; --  
DR HSSP: P04070; lPCU.  
DR MEROPS: S01.218;  
DR InterPro: IPR000152; Asx\_hydroxyl.  
DR InterPro: IPR001314; Chymotrypsin.  
DR InterPro: IPR001881; EGF Ca.  
DR InterPro: IPR006209; EGF-like.  
DR InterPro: IPR002383; GLA\_blood.  
DR InterPro: IPR006210; IEGF.  
DR InterPro: IPR001254; Ser\_protease\_Try.  
DR InterPro: IPR000294; VitK\_dep\_GLA.

DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00594; gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00181; EGF; 2.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; Tryp\_SPC; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Blood coagulation; Glycoprotein; Serine protease;  
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.  
FT SIGNAL 1 18 BY SIMILARITY.  
FT PROPEP 19 41 BY SIMILARITY.  
FT CHAIN 42 459 VITAMIN K-DEPENDENT PROTEIN C.  
FT CHAIN 42 196 PROTEIN C LIGHT CHAIN (BY SIMILARITY).  
FT CHAIN 199 459 PROTEIN C HEAVY CHAIN (BY SIMILARITY).  
FT PEPTIDE 199 213 ACTIVATION PEPTIDE (BY SIMILARITY).  
FT SITE 213 214 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).  
FT DOMAIN 96 131 EGF-LIKE 1.  
FT DOMAIN 135 175 EGF-LIKE 2.  
FT DOMAIN 214 459 SERINE PROTEASE.  
FT MOD\_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
FT MOD\_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
FT MOD\_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
FT MOD\_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
FT MOD\_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
FT MOD\_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
FT MOD\_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
FT MOD\_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
FT MOD\_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
FT MOD\_RES 112 112 HYDROXYLATION (BY SIMILARITY).  
FT ACT\_SITE 255 255 CHARGE RELAY SYSTEM.  
FT ACT\_SITE 301 301 CHARGE RELAY SYSTEM.  
FT ACT\_SITE 400 400 CHARGE RELAY SYSTEM.  
FT DISULFID 58 63 BY SIMILARITY.  
FT DISULFID 91 110 BY SIMILARITY.  
FT DISULFID 100 105 BY SIMILARITY.  
FT DISULFID 104 119 BY SIMILARITY.  
FT DISULFID 121 130 BY SIMILARITY.  
FT DISULFID 139 150 BY SIMILARITY.  
FT DISULFID 146 159 BY SIMILARITY.  
FT DISULFID 161 174 BY SIMILARITY.  
FT DISULFID 182 321 INTERCHAIN (BY SIMILARITY).  
FT DISULFID 240 256 BY SIMILARITY.  
FT DISULFID 371 385 BY SIMILARITY.  
FT DISULFID 396 424 BY SIMILARITY.  
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;

Query Match 61.0%; Score 122; DB 1; Length 459;  
Best Local Similarity 52.3%; Pred. No. 4.8e-13;





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FT ACT SITE 397 397 CHARGE RELAY SYSTEM.
FT DISULFID 56 61 BY SIMILARITY.
FT DISULFID 89 108 BY SIMILARITY.
FT DISULFID 98 103 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 119 128 BY SIMILARITY.
FT DISULFID 137 148 BY SIMILARITY.
FT DISULFID 144 157 BY SIMILARITY.
FT DISULFID 159 172 BY SIMILARITY.
FT DISULFID 180 318 INTERCHAIN.
FT DISULFID 237 253
FT DISULFID 368 382
FT DISULFID 393 421
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .).
FT VARIANT 82 82 F -> K.
FT CONFLICT 455 456 VP -> PV (IN REF. 4).
SQ SEQUENCE 456 AA; 51407 MW; CAA6833F894C209 CRC64;

Query Match 60.5%; Score 121; DB 1; Length 456;
Best Local Similarity 50.0%; Pred. No. 7.1e-13;
Matches 21; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANSFLXLRHGSXRXCXIXXICDPXXAKXIFEDVDVDTLAFWS 42
Db 40 ANSFLEELRPNVERCESEVCFEAREIFQNTEDTMAFWS 81

RESULT 7
FA10_BOVIN STANDARD; PRT; 492 AA.
AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-487 FROM N.A.
RX MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McGillivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence.";
RL Nucleic Acids Res. 12:4481-4492(1984).
RN [2]
RP SEQUENCE OF 41-180.
RX MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor X1 (Stuart
RT factor).";
RL Biochemistry 19:659-667(1980).
RN [3]
RP REVISION TO 103.
RX MEDLINE=93308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kisiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=76053069; PubMed=1055093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor X1 (Stuart factor): amino-acid sequence of heavy
RT chain.";
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Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
[5]
RN SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RL moieties in the activation of factor X.";
Eur. J. Biochem. 218:153-163(1993).
RN [6]
RP ACTIVE SITE.
RX MEDLINE=73053314; PubMed=4264286;
RA Titani K., Hermodson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor X1a (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases.";
RL Biochemistry 11:4899-4903(1972).
RN [7]
RP PROCESSING.
RX MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta.";
Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN [8]
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185716; PubMed=6546930;
RA Sugo T., Bjoerk I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region.";
J. Biol. Chem. 259:5705-5710(1984).
RN [9]
RP SULFATION.
RX MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors X1 and X2 to tyrosine 18 in the activation
RT peptide.";
J. Biol. Chem. 261:4008-4014(1986).
RN [10]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=91084483; PubMed=2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
RT the amino-terminal epidermal growth factor like domain in coagulation
RT factor X.";
Biochemistry 29:8111-8118(1990).
RN [11]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92329412; PubMed=1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Teleman O.;
RT "Three-dimensional structure of the apo form of the N-terminal
RT EGF-like module of blood coagulation factor X as determined by NMR
RT spectroscopy and simulated folding.";
RL Biochemistry 31:5974-5983(1992).
RN [12]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92406922; PubMed=1527084;
RA Selander-Sunnerhagen M., Ullner M., Persson E., Teleman O.,
RA Stenflo J., Drakenberg T.;
RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
RT like domain in coagulation factor X.";
J. Biol. Chem. 267:19642-19649(1992).
RN [13]
RP STRUCTURE BY NMR OF 41-126.
RX MEDLINE=96387194; PubMed=8794734;
RA Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
RA Trewhella J.;
RT "The relative orientation of Gla and EGF domains in coagulation
RT factor X is altered by Ca2+ binding to the first EGF domain. A
RT combined NMR-small angle X-ray scattering study.";
```



RX MEDLINE=83257207; PubMed=6871167;  
 RA McMullen B.A., Fujikawa K., Kistiel W., Saeagawa T., Howald W.N.,  
 RA Kwa E.Y., Weinstein B.;  
 RT "Complete amino acid sequence of the light chain of human blood  
 RT coagulation factor X: evidence for identification of residue 63 as  
 RT beta-hydroxyaspartic acid.";  
 RL Biochemistry 22:2875-2884 (1983).  
 RN [7]  
 RN SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=Liver;  
 RX MEDLINE=84222026; PubMed=6587384;  
 RA Leytus S.P., Chung D.W., Kistiel W., Kurachi K., Davie E.W.;  
 RT "Characterization of a cDNA coding for human factor X.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702 (1984).  
 RN [8]  
 RN SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=94062825; PubMed=8243461;  
 RA Inoue K., Morita T.;  
 RT "Identification of O-linked oligosaccharide chains in the activation  
 RT peptides of blood coagulation factor X. The role of the carbohydrate  
 RT moieties in the activation of factor X.";  
 RL Eur. J. Biochem. 218:153-163 (1993).  
 RN [9]  
 RN SEQUENCE OF 1-23 FROM N.A.  
 RX MEDLINE=90128299; PubMed=2612918;  
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusan K., Lyman G.;  
 RT "Cloning and characterization of the 5' end (exon 1) of the gene  
 RT encoding human factor X.";  
 RL Gene 84:517-519 (1989).  
 RN [10]  
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=93360277; PubMed=8355279;  
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,  
 RA Huber R., Blankenship D.T., Cardin A.D., Kistiel W.;  
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";  
 RL J. Mol. Biol. 232:947-966 (1993).  
 RN [11]  
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=98283982; PubMed=9618463;  
 RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;  
 RT "Structural basis for chemical inhibition of human blood coagulation  
 RT factor Xa.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635 (1998).  
 RN [12]  
 RN VARIANTS ILE-7 AND HIS-30.  
 RX MEDLINE=99318093; PubMed=10391209;  
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemes J., Ziaugra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.Q.,  
 RA Lander E.S.;  
 RT "Characterization of single-nucleotide polymorphisms in coding regions  
 RT of human genes.";  
 RL Nat. Genet. 22:231-238 (1999).  
 RN [13]  
 RN ERRATUM.  
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemes J., Ziaugra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.Q.,  
 RA Lander E.S.;  
 RL Nat. Genet. 23:373-373 (1999).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- PTM: N- AND O-GLYCOSYLATED.

CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: Contains 2 EGF-like domains.  
 CC -----  
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 DR EMBL; K03194; AA52490.1; -;  
 DR EMBL; M57285; AA52421.1; -;  
 DR EMBL; AF503510; AA519347.1; -;  
 DR EMBL; L29433; AA52764.1; -;  
 DR EMBL; L00390; AA52764.1; JOINED.  
 DR EMBL; L00391; AA52764.1; JOINED.  
 DR EMBL; L00392; AA52764.1; JOINED.  
 DR EMBL; L00393; AA52764.1; JOINED.  
 DR EMBL; L00394; AA52764.1; JOINED.  
 DR EMBL; L00395; AA52764.1; JOINED.  
 DR EMBL; L00396; AA52764.1; JOINED.  
 DR EMBL; M22613; AA51984.1; -;  
 DR EMBL; K01886; AA52486.1; -;  
 DR EMBL; M33297; AA52636.1; -;  
 DR PIR; A24478; EXHU.  
 DR PDB; 1HCG; 08-MAY-95.  
 DR PDB; 1FAX; 29-OCT-97.  
 DR PDB; 1FXV; 17-JUN-98.  
 DR PDB; 1XXA; 23-MAR-99.  
 DR PDB; 1XXB; 23-MAR-99.  
 DR PDB; 1EQZ; 20-SEP-00.  
 DR PDB; 1FOR; 20-SEP-00.  
 DR PDB; 1FOS; 20-SEP-00.  
 DR PDB; 1FUS; 17-NOV-00.  
 DR PDB; 1G2L; 20-OCT-01.  
 DR PDB; 1G2M; 20-OCT-01.  
 DR PDB; 1KSN; 19-JUN-02.  
 DR PDB; 1KYB; 11-FEB-03.  
 DR PDB; 1MQ5; 28-JAN-03.  
 DR PDB; 1MO6; 28-JAN-03.  
 DR PDB; 1NEU; 25-FEB-03.  
 DR PDB; 1NEW; 25-FEB-03.  
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 DR PDB; 1NFI; 25-FEB-03.  
 DR MEROPS; S01.216; -;  
 DR GlycoSuiteDB; P00742; -;  
 DR Genew; HGNC:3528; F10.  
 DR MIM; 134530; -;  
 DR MIM; 227600; -;  
 DR GO; GO:0005576; C:extracellular; TAS.  
 DR GO; GO:0003804; F:blood coagulation factor X activity; TAS.  
 DR GO; GO:0007596; P:blood coagulation; TAS.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001438; EGF\_II.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00594; Gla; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00010; EGFBL00D.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.



DR PROSITE; PS00022; EGF 1; 1.  
 DR PROSITE; PS01186; EGF 2; 2.  
 DR PROSITE; PS01187; EGF CA; 1.  
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.  
 DR PROSITE; PS00240; TRYPSIN DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN SER; 1.  
 KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;  
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 KW Signal; Zymogen; EGF-like domain; Repeat.  
 FT SIGNAL 1 20  
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 FT PROPEP 184 232  
 FT CHAIN 233 490  
 FT DOMAIN 86 122  
 FT DOMAIN 125 165  
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 FT CARBOHYD 187 187  
 FT CARBOHYD 205 205  
 SQ SEQUENCE 490 AA; 53965 MW; 3A39FA85AF2A6D11 CRC64;

Query Match 50.5%; Score 101; DB 1; Length 490;  
 Best Local Similarity 43.2%; Pred. No. 2.1e-09;  
 Matches 19; Conservative 8; Mismatches 17; Indels 0; Gaps 0;  
 QY 1 ANSGLXLRHSGSLKRXCIIXICDFXXAKXIFEDVDDTLAFMSKH 44  
 DB 41 ANSFLLEKKGKGNLRECMENCSYEALFVEDREKTNFQWKY 84

RESULT 11

FA7\_RABIT ID FA7\_RABIT STANDARD; PRT; 444 AA.  
 AC P98139; P92224;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin  
 GN conversion accelerator).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA MEDLINE=93190306; PubMed=8383365;  
 RX Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;  
 RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation  
 RL factor VII."; Suppl. 69:231-238(1993).  
 RN [2]  
 RP REVISION TO 395.  
 RC TISSUE=Liver;  
 RA Ruiz S.R., Blajchman M.A., Clarke B.J.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZIMOGEN FORM. FACTOR VII IS  
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR  
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR XA  
 CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR IXA  
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO  
 CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY  
 CC SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to  
 CC form factor Xa.  
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 CC BY A DISULFIDE BOND (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: Plasma.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: Contains 2 EGF-like domains.  
 CC -----  
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 CC -----  
 DR EMBL; U77477; AAB37326.1; -.  
 DR HSSP; P08709; 1FAK.  
 DR MEROPS; S01.215; -.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001438; EGF\_II.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00594; gla; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00010; EGF\_BLOOD.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
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 DR SMART; SM00020; Tryp\_Spc; 1.















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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:16:11 ; Search time 34 Seconds  
(without alignments)  
333.950 Million cell updates/sec

Title: US09497591-LEDITED

Perfect score: 200

Sequence: 1 ANSFLXLRHGLRXCIXX.....XXAKIFEDVDTLAFWSKH 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL.23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	150	75.0	456	6 Q9TTR0	Q9TTR0 canis famil
2	139	69.5	460	11 Q91WN8	Q91WN8 mus musculu
3	133	66.5	460	11 Q99PC6	Q99PC6 mus musculu
4	126	63.0	55	4 Q8J002	Q8J002 homo sapien
5	126	63.0	55	4 Q81XB5	Q81XB5 homo sapien
6	113	56.5	482	11 Q63207	Q63207 rattus norv
7	102.5	51.2	443	13 Q8JHC9	Q8JHC9 brachydanio
8	102	51.0	231	4 Q8N2N6	Q8N2N6 homo sapien
9	99	49.5	481	11 Q54740	Q54740 mus musculu
10	99	49.5	481	11 Q99L32	Q99L32 mus musculu
11	99	49.5	481	11 Q88947	Q88947 mus musculu
12	98	49.0	701	4 Q96PQ8	Q96PQ8 homo sapien
13	95	47.5	474	13 Q8JHC8	Q8JHC8 brachydanio
14	93	46.5	469	6 Q9GMD9	Q9GMD9 ornithorhyn
15	88	44.0	229	13 Q8J40	Q8J40 xenopus lae
16	87	43.5	268	4 Q8NEK6	Q8NEK6 homo sapien

ALIGNMENTS

RESULT 1

Q9TTR0 PRELIMINARY; PRT; 456 AA.

ID Q9TTR0; AC Q9TTR0; DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Protein C precursor.  
GN PROC.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.  
RA Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunnberg L.,  
RA Brenig B.;  
RT "Molecular characterization and chromosomal assignment of the canine  
protein C gene."  
RL Mamm. Genome 10:135-139(1999).  
RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE-93171952; PubMed-10443005;  
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;  
RT "Analysis of canine protein C gene polymorphisms."  
RL Anim. Genet. 30:237-238(1999).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
DR EMBL; AJ001979; CAA05126.1; -;  
DR HSSP; P04070; 1AUT.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00594; gla; 1.

P83370 hoplocephal  
Q15253 homo sapien  
Q16519 homo sapien  
Q9nsd0 homo sapien  
Q61109 mus musculu  
Q8t613 halocynthia  
Q82994 sus scrofa  
Q91001 gallus gall  
Q8k3u6 rattus norv  
Q14316 homo sapien  
Q95nd7 pan troglod  
Q95nd6 pan troglod  
Q29094 sus scrofa  
Q8jhd0 brachydanio  
Q9yvk1 brachydanio  
Q95ne8 bos taurus  
Q8ixd5 homo sapien  
P82807 notechis sc  
Q9ptw7 struthio ca  
Q8ixc5 homo sapien  
Q8ci01 mus musculu  
Q9cqw3 mus musculu  
Q8bm25 mus musculu  
Q8bgn6 mus musculu  
Q9gvh6 rattus sp.  
Q8tae3 homo sapien  
Q8rl82 mus musculu  
Q8aye4 brachydanio  
Q61592 mus musculu



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Q8J002
ID Q8J002 PRELIMINARY; PRT; 55 AA.
AC Q8J002;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Protein C (Fragment).
GN PROC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kinoshita S., Iida H., Inoue S., Watanabe K., Kurihara M., Wada Y.,
RA Ono M., Dongchon K., Hamasaki N.;
RT "Gene Analysis of Anticoagulation Factors in Japanese Thrombotic
RT Patients: Genetic Background of Thrombophilia in Japan.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083700; BAC21172.1; -.
FT NON_TER 1
FT NON_TER 55
SQ SEQUENCE 55 AA; 6527 MW; 4F89496534A78836 CRC64;

Query Match 63.0%; Score 126; DB 4; Length 55;
Best Local Similarity 67.6%; Pred. No. 1e-13;
Matches 25; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRCIXIXICDPXXAKXIFEDVDDT 37
DB 19 ANSFLKRLHSSLERECIEICDFEAKEIFQNVDDT 55

RESULT 5
Q8IXB5 PRELIMINARY; PRT; 55 AA.
AC Q8IXB5;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Protein C (Fragment).
GN PROC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamasaki S., Kang D., Kinoshita S., Iida K., Inoue S., Watanabe K.,
RA Kurihara M., Wada Y., Ono M.;
RT "Gene analysis of anticoagulation factors in Japanese thrombotic
RT patients: Genetic background of thrombophilia in Japan.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086851; BAC53631.1; -.
FT NON_TER 1
FT NON_TER 55
SQ SEQUENCE 55 AA; 6475 MW; 3803696534BC9289 CRC64;

Query Match 63.0%; Score 126; DB 4; Length 55;
Best Local Similarity 67.6%; Pred. No. 1e-13;
Matches 25; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRCIXIXICDPXXAKXIFEDVDDT 37
DB 19 ANSFLKRLHSSLERECIEICDFEAKEIFQNVDDT 55

RESULT 6
Q63207 PRELIMINARY; PRT; 482 AA.
AC Q63207;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
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DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STATON C., ROSS R.P., HUTSON S., WALLIN R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase.";
RL Thromb. Res. 80:63-73(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; X79807; CAAS6202.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001891; EGF_Ca.
DR InterPro; IPR001438; EGF_I1.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR001254; Ser. protease Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR0010; EGF_BLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 482 AA; 54265 MW; 0284670E3954A698 CRC64;

Query Match 56.5%; Score 113; DB 11; Length 482;
Best Local Similarity 43.2%; Pred. No. 1.7e-10;
Matches 19; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRCIXIXICDPXXAKXIFEDVDDTLAFWSKH 44
DB 41 ANSFPEIKKGNLERECVEICSFEEAREVFEDNEKTEFWNKY 84

RESULT 7
Q8JHC9 PRELIMINARY; PRT; 443 AA.
AC Q8JHC9;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Coagulation factor VIII.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Hanumanthiah R., Day K., Jagadeeswaran P.;
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=98347933; PubMed=9684791;
RL Liang Z., Cooper A., DeFord M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
FT factor X.";
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129SvJ;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and Characterization of the Murine Factor X Gene.";
RL Thromb. Haemost. 0:0-0(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR ENBL; AF087644; AAC36345.1; -.
DR ENBL; AF211347; AAF22980.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01_215; -.
DR MGD; MG1:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla_1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGF_BLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR EGF-like domain; HydrolasE; Protease; Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 54018 MW; 8AC09DE5EF9D271E CRC64;

Query Match 49.5%; Score 99; DB 11; Length 481;
Best Local Similarity 38.6%; Pred No. 4e-08;
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gap

Qy 1 ANSFLXLLRHGSLRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
||||| : ||| : ||| : ||| : ||| : ||| :
Db 41 ANSFPEEPKGNLERECMEIICSVEEVREIFEDDEKTKYWTKY 84

RESULT 12
Q96P08
ID Q96P08 PRELIMINARY; PRT; 701 AA.
AC Q96P08;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Factor VII active site mutant immunoconjugate.
OS Homo sapiens (Human).

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DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA_1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 469 AA; 52196 MW; 4C66C230D0758F6A CRC64;

Query Match 46.5%; Score 93; DB 6; Length 469;
Best Local Similarity 40.5%; Pred.No. 4.le-07;
Matches 17; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSXRCXCIXXICDPXXAKXIFEDVDDTLAFWS 42
DB 41 ANSLFELKGNLERECNEETCSYEAREVFEDTDKTNEFWN 82

RESULT 15
Q8JJ40 PRELIMINARY; PRT; 229 AA.
AC Q8JJ40;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Mitotic phosphoprotein 77 (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21676254; PubMed=11818060;
RA Georgi A.B., Stukenberg P.T., Kirschner M.W.;
RT "Timing of events in mitosis.";
RL Curr. Biol. 12:105-114(2002).
DR ENBL; AF419154; AAM33249.1;
DR InterPro; IPR002383; GLA_blood.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
FT NON_TER 229
SQ SEQUENCE 229 AA; 25543 MW; 42A2856B9AEA6A99 CRC64;

Query Match 44.0%; Score 88; DB 13; Length 229;
Best Local Similarity 34.1%; Pred.No. 1.3e-06;
Matches 15; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSXRCXCIXXICDPXXAKXIFEDVDDTLAFWSKH 44
DB 21 ANSFLERIKQNIERECKELCTVEAREAFENDEKTFNEFWKEY 64

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:17:31 ; Search time 21 Seconds  
(without alignments)  
88.651 Million cell updates/sec

Title: US09497591-1EDITED  
Perfect score: 200  
Sequence: 1 ANSFLXLRHGSLSRXCIIX.....XXAKXIFEDVDTLAFWSKH 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2.6/prodata/1/iaa/6A COMB.pep.\*  
4: /cgn2.6/prodata/1/iaa/6B COMB.pep.\*  
5: /cgn2.6/prodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2.6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	176	88.0	44	3	US-08-955-636-19
2	174	87.0	44	3	US-08-955-636-24
3	174	87.0	44	3	US-08-955-636-35
4	168	84.0	44	3	US-08-955-636-1
5	168	84.0	44	3	US-08-955-636-20
6	168	84.0	44	3	US-08-955-636-21
7	168	84.0	44	3	US-08-955-636-25
8	168	84.0	44	2	US-08-965-832-2
9	168	84.0	419	1	US-08-295-411-1
10	168	84.0	419	2	US-08-955-471-1
11	168	84.0	419	4	US-09-667-570A-3
12	168	84.0	419	5	PCT-US92-10242-1
13	168	84.0	460	2	US-08-756-506-2
14	168	84.0	460	2	US-08-756-506-4
15	168	84.0	460	6	5270178-13
16	168	84.0	460	6	5270178-14
17	168	84.0	460	6	5270178-15
18	168	84.0	460	6	5270178-16
19	168	84.0	461	6	5225537-2
20	168	84.0	461	6	5270178-17
21	168	84.0	461	6	5270178-18
22	168	84.0	461	6	5460953-3
23	167	83.5	44	3	US-08-955-636-22
24	155	77.5	42	2	US-08-745-254A-2
25	155	77.5	461	6	5270178-2
26	151	75.5	41	1	US-08-229-280-5
27	137	68.5	410	3	US-09-065-872-1

28	137	68.5	410	4	US-09-667-570A-1	Sequence 1, Appli
29	129	64.5	409	3	US-09-065-872-2	Sequence 2, Appli
30	129	64.5	409	4	US-09-667-570A-2	Sequence 2, Appli
31	125	62.5	44	3	US-08-955-636-23	Sequence 23, Appli
32	115	57.5	44	3	US-08-955-636-2	Sequence 2, Appli
33	112	56.0	139	1	US-08-330-978-2	Sequence 2, Appli
34	112	56.0	139	1	US-08-474-042-2	Sequence 2, Appli
35	112	56.0	139	1	US-08-484-558-2	Sequence 2, Appli
36	112	56.0	139	1	US-08-774-592-2	Sequence 2, Appli
37	112	56.0	437	1	US-08-487-037-2	Sequence 2, Appli
38	112	56.0	437	1	US-08-487-037-3	Sequence 3, Appli
39	112	56.0	488	1	US-08-487-037-1	Sequence 1, Appli
40	109	54.5	487	1	US-08-469-486-53	Sequence 53, Appli
41	109	54.5	487	2	US-08-469-486-53	Sequence 53, Appli
42	109	54.5	492	1	US-08-469-486-2	Sequence 2, Appli
43	109	54.5	492	2	US-08-469-486-2	Sequence 2, Appli
44	108	54.0	448	1	US-08-295-411-3	Sequence 3, Appli
45	108	54.0	448	2	US-08-955-471-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-08-955-636-19  
; Sequence 19, Application US/08955636A  
; Patent No. 6017882  
; GENERAL INFORMATION:  
; APPLICANT: Nelsestuen, Gary  
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
; FILE OF INVENTION: POLYPEPTIDES  
; FILE REFERENCE: 09531/002001  
; CURRENT APPLICATION NUMBER: US/08/955,636A  
; CURRENT FILING DATE: 1997-10-23  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-19

Query Match 88.0%; Score 176; DB 3; Length 44;  
Best Local Similarity 97.7%; Pred. No. 1.6e-22;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ANSFLXLRHGSLSRXCIIXICDXXXXKXIFEDVDTLAFWSKH 44  
DB 1 ANSFLXLRHGSLSRXCIIXICDXXXXKXIFEDVDTLAFWSKH 44

RESULT 2  
US-08-955-636-24  
; Sequence 24, Application US/08955636A  
; Patent No. 6017882  
; GENERAL INFORMATION:  
; APPLICANT: Nelsestuen, Gary  
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
; FILE OF INVENTION: POLYPEPTIDES  
; FILE REFERENCE: 09531/002001  
; CURRENT APPLICATION NUMBER: US/08/955,636A  
; CURRENT FILING DATE: 1997-10-23  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 24  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:

; NAME/KEY: MOD RES  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-24

Query Match 87.0%; Score 174; DB 3; Length 44;  
Best Local Similarity 97.7%; Pred. No. 3.5e-22;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44  
Db 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

## RESULT 3

US-08-955-636-35  
; Sequence 35; Application US/08955636A

; Patent No. 6017882

; GENERAL INFORMATION:

; APPLICANT: Nelstuen, Gary

; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

; FILE REFERENCE: 09531/002001

; CURRENT APPLICATION NUMBER: US/08/955,636A

; CURRENT FILING DATE: 1997-10-23

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 35

; LENGTH: 44

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (0)...(0)

; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-35

Query Match 87.0%; Score 174; DB 3; Length 44;  
Best Local Similarity 97.7%; Pred. No. 3.5e-22;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44  
Db 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

## RESULT 4

US-08-955-636-1

; Sequence 1; Application US/08955636A

; Patent No. 6017882

; GENERAL INFORMATION:

; APPLICANT: Nelstuen, Gary

; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

; FILE REFERENCE: 09531/002001

; CURRENT APPLICATION NUMBER: US/08/955,636A

; CURRENT FILING DATE: 1997-10-23

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 44

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (0)...(0)

; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-1

Query Match 84.0%; Score 168; DB 3; Length 44;  
Best Local Similarity 93.2%; Pred. No. 3.5e-21;  
Matches 41; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44  
Db 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFQNVDDTLAFWSKH 44

## RESULT 5

US-08-955-636-20

; Sequence 20; Application US/08955636A

; Patent No. 6017882

; GENERAL INFORMATION:

; APPLICANT: Nelstuen, Gary

; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

; FILE REFERENCE: 09531/002001

; CURRENT APPLICATION NUMBER: US/08/955,636A

; CURRENT FILING DATE: 1997-10-23

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 20

; LENGTH: 44

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (0)...(0)

; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-20

Query Match 84.0%; Score 168; DB 3; Length 44;  
Best Local Similarity 95.5%; Pred. No. 3.5e-21;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44  
Db 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

## RESULT 6

US-08-955-636-21

; Sequence 21; Application US/08955636A

; Patent No. 6017882

; GENERAL INFORMATION:

; APPLICANT: Nelstuen, Gary

; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

; FILE REFERENCE: 09531/002001

; CURRENT APPLICATION NUMBER: US/08/955,636A

; CURRENT FILING DATE: 1997-10-23

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 21

; LENGTH: 44

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (0)...(0)

; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-21

Query Match 84.0%; Score 168; DB 3; Length 44;  
Best Local Similarity 95.5%; Pred. No. 3.5e-21;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44  
Db 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

## RESULT 7

US-08-955-636-25

; Sequence 25; Application US/08955636A

; Patent No. 6017882

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; GENERAL INFORMATION:
; APPLICANT: Nelsetuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-25

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Query Match      84.0%; Score 168; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 3.5e-21;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 ANSFLXLRHGSIXRCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXLRHSSLRXRCIXXICDFXXAPXIFEDVDDTLAFWSKH 44

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RESULT 8
US-08-965-832-2
; Sequence 2, Application US/08965832
; Patent No. 5847085
; GENERAL INFORMATION:
; APPLICANT: CHARLES T. ESMON AND MIKHAIL D. SMIRNOV
; TITLE OF INVENTION: Modified Protein C
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,832
; FILING DATE: 7-NOV-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/745,254
; FILING DATE: 8-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,768
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF 165/167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

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; FEATURE:
; NAME/KEY:
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29
; OTHER INFORMATION: /note= "where Xaa means gamma
; OTHER INFORMATION: carboxylglutamic acid"
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: /note= "partial sequence of human protein C"
US-08-965-832-2

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Query Match      84.0%; Score 168; DB 2; Length 45;
Best Local Similarity 93.2%; Pred. No. 3.6e-21;
Matches 41; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 ANSFLXLRHGSIXRCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXLRHSSLRXRCIXXICDFXXAKXIFQNVDDTLAFWSKH 44

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RESULT 9
US-08-295-411-1
; Sequence 1, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffen, John H.
; APPLICANT: Meesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..157
; OTHER INFORMATION: /note= "Protein C Light Chain"
; FEATURE:
; NAME/KEY: Region

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/ FILING DATE: 19921118
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/793,989
/ FILING DATE: 18-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: SCR0472P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-554-2937
/ TELEFAX: 619-554-6312
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 419 amino acids
/ TYPE: AMINO ACID
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 1..157
/ OTHER INFORMATION: /note= "Protein C Light Chain"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 158..169
/ OTHER INFORMATION: /note= "Protein C Activation"
/ OTHER INFORMATION: Peptide"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 170..419
/ OTHER INFORMATION: /note= "Protein C Heavy Chain"
PCT-US92-10242-1
Query Match 84.0%; Score 168; DB 5; Length 419;
Best Local Similarity 72.7%; Pred. No. 4.4e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
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QY 1 ANSFLXLRHSGSLXRCIXXICDPYXAXXIFEDVDDTLAFWSKH 44
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DB 1 ANSFLELRHSLRECEIEICDFEAKEIFQNVDDTLAFWSKH 44
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RESULT 13
US-08-756-506-2
; Sequence 2, Application US/08756506
; Patent No. 5905185
; GENERAL INFORMATION:
; APPLICANT: Garner, Ian
; APPLICANT: Cottingham, Ian R.
; APPLICANT: Temperley, Simon M.
; APPLICANT: Foster, Donald C.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Prunkard, Donna E.
; TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,506
; FILING DATE:
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/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sawislak, Deborah A
/ REGISTRATION NUMBER: 37,438
/ REFERENCE/DOCKET NUMBER: 95-28
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-442-6672
/ TELEFAX: 206-442-6678
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 460 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-756-506-2
Query Match 84.0%; Score 168; DB 2; Length 460;
Best Local Similarity 72.7%; Pred. No. 4.9e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSGSLXRCIXXICDPYXAXXIFEDVDDTLAFWSKH 44
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DB 43 ANSFLELRHSLRECEIEICDFEAKEIFQNVDDTLAFWSKH 86

RESULT 14
US-08-756-506-4
; Sequence 4, Application US/08756506
; Patent No. 5905185
; GENERAL INFORMATION:
; APPLICANT: Garner, Ian
; APPLICANT: Cottingham, Ian R.
; APPLICANT: Temperley, Simon M.
; APPLICANT: Foster, Donald C.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Prunkard, Donna E.
; TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,506
; FILING DATE:
; CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sawislak, Deborah A
/ REGISTRATION NUMBER: 37,438
/ REFERENCE/DOCKET NUMBER: 95-28
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-442-6672
/ TELEFAX: 206-442-6678
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 460 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-756-506-4
Query Match 84.0%; Score 168; DB 2; Length 460;
Best Local Similarity 72.7%; Pred. No. 4.9e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
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QY 1 ANSFLXXLRHGSIXXICDXXAKXIFEDVDDTLAFWSKH 44
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Db 43 ANSFLEELRHSSLERECIEICDFEAKEIFQNVDDTLAFWSKH 86

RESULT 15
5270178-13
; Patent No. 5270178
; APPLICANT: GERLITZ, BRUCE E.; GRINNELL, BRIAN W.
; TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF
; ZMOGEN FORMS OF HUMAN PROTEIN C
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/484,133
; FILING DATE: 23-FEB-1990
; SEQ ID NO:13:
; LENGTH: 460
5270178-13

Query Match      84.0%; Score 168; DB 6; Length 460;
Best Local Similarity 72.7%; Pred. No. 4.9e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXXICDXXAKXIFEDVDDTLAFWSKH 44
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Db 43 ANSFLEELRHSSLERECIEICDFEAKEIFQNVDDTLAFWSKH 86

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Search completed: December 30, 2003, 09:20:38  
Job time : 22 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:19:36 ; Search time 31 Seconds  
(without alignments)

282.476 Million cell updates/sec

Title: US09497591-LEDITED

Perfect score: 200

Sequence: 1 ANSFLXLRHSLXRCIXX.....XXAKXIFEDVDTLAFWSKH 44

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Maximum Match 100%

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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
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- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	182	91.0	419	12	US-10-168-407-3
2	182	91.0	419	12	US-10-168-407-4
3	182	91.0	419	15	US-10-182-263-3
4	182	91.0	419	15	US-10-182-263-4
5	182	91.0	419	15	US-10-182-263-5
6	174	87.0	419	12	US-10-168-407-5
7	174	87.0	419	12	US-10-168-407-6
8	174	87.0	419	15	US-10-182-263-6
9	168	84.0	44	15	US-10-298-330-1
10	168	84.0	419	11	US-09-978-917A-4
11	168	84.0	419	12	US-10-168-407-1
12	168	84.0	419	15	US-10-182-263-1
13	168	84.0	461	11	US-09-978-917A-2
14	168	84.0	461	12	US-10-168-407-2
15	168	84.0	461	15	US-10-182-263-2

16	115	57.5	44	15	US-10-298-330-2	Sequence 2, Appli
17	108	54.0	488	12	US-10-348-504-44	Sequence 44, Appl
18	108	54.0	488	12	US-10-407-123-27	Sequence 27, Appl
19	101	50.5	44	15	US-10-298-330-18	Sequence 18, Appl
20	98	49.0	406	11	US-03-782-587B-3	Sequence 3, Appli
21	98	49.0	466	12	US-10-375-741-14	Sequence 14, Appl
22	98	49.0	466	15	US-10-017-122-2	Sequence 2, Appli
23	95	47.5	44	15	US-10-298-330-3	Sequence 3, Appli
24	95	47.5	406	11	US-09-782-587B-1	Sequence 1, Appli
25	95	47.5	406	12	US-10-386-898-7	Sequence 7, Appli
26	95	47.5	406	15	US-10-109-498-1	Sequence 1, Appli
27	95	47.5	406	15	US-10-255-032-1	Sequence 1, Appli
28	95	47.5	406	16	US-10-281-727-1	Sequence 1, Appli
29	89	44.5	44	15	US-10-298-330-4	Sequence 4, Appli
30	86	43.0	40	15	US-10-298-330-23	Sequence 23, Appl
31	84	42.0	40	15	US-10-298-330-22	Sequence 22, Appl
32	84	42.0	40	15	US-10-298-330-25	Sequence 25, Appl
33	84	42.0	96	11	US-09-759-130B-313	Sequence 313, App
34	84	42.0	96	12	US-10-188-495-43	Sequence 43, Appl
35	84	42.0	96	15	US-10-189-123-43	Sequence 43, Appl
36	84	42.0	209	11	US-09-759-130B-312	Sequence 312, App
37	84	42.0	209	12	US-10-188-495-42	Sequence 42, Appl
38	84	42.0	209	15	US-10-189-123-42	Sequence 42, Appl
39	84	42.0	226	11	US-09-759-130B-310	Sequence 310, App
40	84	42.0	226	12	US-10-188-495-40	Sequence 40, Appl
41	84	42.0	226	15	US-10-189-123-40	Sequence 40, Appl
42	82	41.0	40	15	US-10-298-330-24	Sequence 24, Appl
43	82	41.0	622	15	US-10-020-141-8	Sequence 8, Appli
44	82	41.0	622	15	US-10-017-631-2	Sequence 2, Appli
45	82	41.0	622	15	US-10-214-932-116	Sequence 116, App

#### ALIGNMENTS

RESULT 1

US-10-168-407-3  
; Sequence 3, Application US/10168407  
; Publication No. US20030207435A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerlitz, Bruce E  
; TITLE OF INVENTION: PROTEIN C DERIVATIVES  
; FILE REFERENCE: X-13610  
; CURRENT APPLICATION NUMBER: US/10/168,407  
; CURRENT FILING DATE: 2002-11-04  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 3  
; LENGTH: 419  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-168-407-3

Query Match 91.0%; Score 182; DB 12; Length 419;  
Best Local Similarity 79.5%; Pred. No. 3.2e-22;  
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSLXRCIXXICDXXAKXIFEDVDTLAFWSKH 44

DB 1 ANSFLXLRHSLXRCIXXICDXXAKXIFEDVDTLAFWSKH 44

RESULT 2

US-10-168-407-4  
; Sequence 4, Application US/10168407  
; Publication No. US20030207435A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerlitz, Bruce E  
; TITLE OF INVENTION: PROTEIN C DERIVATIVES  
; FILE REFERENCE: X-13610  
; CURRENT APPLICATION NUMBER: US/10/168,407

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; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-407-4

Query Match
Best Local Similarity 91.0%; Score 182; DB 12; Length 419;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 3
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan W
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match
Best Local Similarity 91.0%; Score 182; DB 15; Length 419;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 4
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan W
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match
Best Local Similarity 91.0%; Score 182; DB 15; Length 419;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 5
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan W
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

Query Match
Best Local Similarity 91.0%; Score 182; DB 15; Length 419;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 6
US-10-168-407-5
; Sequence 5, Application US/10168407
; Publication No. US20030207435A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan W
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13610
; CURRENT APPLICATION NUMBER: US/10/168,407
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-407-5

Query Match
Best Local Similarity 87.0%; Score 174; DB 12; Length 419;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 7
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Query Match 84.0%; Score 168; DB 12; Length 419;  
Best Local Similarity .72.7%; Pred. No. 7.3e-20;

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Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1. ANSFLXLRHGSIXRCIXXICDFFXKXKXIFEDVDDTLAFWSKH 44
Db 1. ANSFLELRHSSLRERCIEICDFEAKEIFQNVDDTLAFWSKH 44

RESULT 12
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match 84.0%; Score 168; DB 15; Length 419;
Best Local Similarity 72.7%; Pred. No. 7.3e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1. ANSFLXLRHGSIXRCIXXICDFFXKXKXIFEDVDDTLAFWSKH 44
Db 1. ANSFLELRHSSLRERCIEICDFEAKEIFQNVDDTLAFWSKH 44

RESULT 13
US-09-978-917A-2
; Sequence 2, Application US/09978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219us310 - protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(42)
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (43)...(461)
US-09-978-917A-2

Query Match 84.0%; Score 168; DB 11; Length 461;
Best Local Similarity 72.7%; Pred. No. 8.1e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1. ANSFLXLRHGSIXRCIXXICDFFXKXKXIFEDVDDTLAFWSKH 44
Db 43. ANSFLELRHSSLRERCIEICDFEAKEIFQNVDDTLAFWSKH 86
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RESULT 14
US-10-168-407-2
; Sequence 2, Application US/10168407
; Publication No. US20030207435A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13610
; CURRENT APPLICATION NUMBER: US/10/168,407
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-407-2

Query Match 84.0%; Score 168; DB 12; Length 461;
Best Local Similarity 72.7%; Pred. No. 8.1e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1. ANSFLXLRHGSIXRCIXXICDFFXKXKXIFEDVDDTLAFWSKH 44
Db 43. ANSFLELRHSSLRERCIEICDFEAKEIFQNVDDTLAFWSKH 86

RESULT 15
US-10-182-263-2
; Sequence 2, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-2

Query Match 84.0%; Score 168; DB 15; Length 461;
Best Local Similarity 72.7%; Pred. No. 8.1e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1. ANSFLXLRHGSIXRCIXXICDFFXKXKXIFEDVDDTLAFWSKH 44
Db 43. ANSFLELRHSSLRERCIEICDFEAKEIFQNVDDTLAFWSKH 86

Search completed: December 30, 2003, 09:25:02
Job time : 32 secs
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